

IN THE CLAIMS

1. (Previously Presented) A method of sequencing a polymer comprising:
 - a) dividing a polymer sample into a number of polymer subsamples, wherein there is a polymer subsample created for each type of monomer present in the polymer sample, wherein only one of the monomer types in each polymer subsample is labeled, and wherein both labeled and unlabeled instances of the one monomer type are incorporated in the polymer subsample;
 - b) sequentially separating each monomer from the polymer subsample;
 - c) detecting the labels of each separated labeled monomer as a function of time;
 - d) constructing a time map for each monomer type in each polymer subsample; and
 - e) assembling the time maps into a polymer sequence.
2. (Original) The method of claim 1 wherein the polymer is a nucleic acid, the monomer is a nucleotide, and the number of polymer subsamples and different monomer types is four.
3. (Original) The method of claim 2, wherein each subsample comprises from about 1000 to about 100,000 copies of the nucleic acid.
4. (Original) The method of claim 2, wherein the labels are bulky groups.
5. (Cancelled)
6. (Previously Presented) The method of claim 2, further comprising attaching the polymer subsample to a surface.
7. (Cancelled).
8. (Previously Presented) The method of claim 1 wherein the polymer is a nucleic acid and sequentially separating each monomer from the polymer subsample is done by an enzyme that has exonuclease activity.
9. (Original) The method of claim 1 wherein detecting the time between labels is accomplished/measured with a time-gated detection device.

10. (Previously Presented) The method of claim 9, wherein the detection device is an optical device.

11. (Original) The method of claim 1, wherein constructing monomer time maps of each of the polymer subsamples comprises analyzing the measured time by overlapping data analysis and frequency analysis to construct the time maps.

12. (Original) The method of claim 1, wherein assembling monomer time maps into a polymer sequence comprises minimum non-overlapping data analysis.

13.-29. (Canceled)